A temporal model of cervicovaginal microbiota identifies targets to promote reproductive health

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Abstract

Cervicovaginal bacterial communities are closely linked to reproductive health. Communities characterized by diverse anaerobes and low *Lactobacillus* abundance are associated with preterm birth, infertility, and risk of sexually transmitted infections (STIs). Women in South Africa are more likely to have these 'high-risk' bacterial communities than women in the U.S. and Europe. But the transition between high- and low-risk community states is not well understood. To examine this, researchers profiled the cervicovaginal bacterial communities of healthy young Black South African women over time. They developed a Markov-based model of transition dynamics that accurately predicted bacterial composition in a separate cross-sectional cohort. While communities with high levels of *Lactobacillus* spp. are usually considered low risk for adverse health outcomes, this model suggested that *Lactobacillus iners*-dominant communities have a higher probability of transitioning to high-risk states than *Lactobacillus crispatus*-dominant ones. Thus, simulations based on the model predict that manipulating the movement between these two community types in favor of *Lactobacillus crispatus* would increase the prevalence of low-risk communities. While these findings are computationally based and require experimental confirmation, they may lead to intervention strategies to reduce bacteria-associated adverse reproductive outcomes for women in sub-Saharan Africa.